

# SEQUENCE LISTING

<110> Mahajan, Pramod B.  
Tagliani, Laura

<120> Rad23 Genes and Uses Thereof

<130> 0964D

<150> 09/413,574

<151> 1999-10-06

<150> 60/109,728

<151> 1998-11-23

<160> 5

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1522

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (58) ... (1272)

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cgacccacgc gtccggtgag gagtgagagt tcaaggaccg aggcggcgctc gggcgag atg  
60

Met

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aag ctt aac gtc aag acc ctc aag ggc acc aac ttc gag atc gag gcg 108  
Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu Ala  
5 10 15

agc ccc gat gca tcg gtt gct gat gtg aag agg atc att gag acc act 156  
Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr Thr  
20 25 30

caa ggt cag agt acc tac cgg gcg gac cag caa atg ctc ata tac caa 204  
Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr Gln  
35 40 45

ggg aaa att ctc aag gat gaa acc act ttg gaa agc aac gga gtt gct 252  
Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val Ala  
50 55 60 65

gag aac agc ttc ctt gtt ata atg ttg tcc aag gct aag gca tca tcg 300  
Glu Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser Ser  
70 75 80

agt gga gct tct acc gct act act gca aaa gct cct gca act ctg gcc 348  
Ser Gly Ala Ser Thr Ala Thr Thr Ala Lys Ala Pro Ala Thr Leu Ala  
85 90 95

caa cct gct gcc cct gtg gcc cct gct gca tca gtt gca aga aca cca 396  
Gln Pro Ala Ala Pro Val Ala Pro Ala Ala Ser Val Ala Arg Thr Pro

100	105	110	
aca cag gct cct gtt gcc	aca gct gaa acg gca	cct cca agt gtc caa	444
Thr Gln Ala Pro Val Ala	Thr Ala Glu Thr Ala	Pro Pro Ser Val Gln	
115	120	125	
cct cag gct gct cca gct	gct acg gtt gct gct	act gat gat gct gat	492
Pro Gln Ala Ala Pro Ala	Ala Thr Val Ala Ala	Thr Asp Asp Ala Asp	
130	135	140	145
gtg tac agt cag gca gct	tca aac ctt gta ttt	ggc aac aat cta gaa	540
Val Tyr Ser Gln Ala Ala	Ser Asn Leu Val Phe	Gly Asn Asn Leu Glu	
150	155	160	
cag act atc caa caa att	ctt gac atg ggt ggt	ggt aca tgg gaa cgt	588
Gln Thr Ile Gln Gln Ile	Leu Asp Met Gly Gly	Gly Thr Trp Glu Arg	
165	170	175	
gat act gtt gtt cgt gct	cta cgt gct gca tac	aat aac ccc gag aga	636
Asp Thr Val Val Arg Ala	Leu Arg Ala Ala Tyr	Asn Asn Pro Glu Arg	
180	185	190	
gct ata gac tac ctg tat	tct gga att cct gag	aat gtg gag gct cag	684
Ala Ile Asp Tyr Leu Tyr	Ser Gly Ile Pro Glu	Asn Val Glu Ala Gln	
195	200	205	
cct gtt gcc cga gca cct	gct gct ggc caa caa	aca aat cag cag gcc	732
Pro Val Ala Arg Ala Pro	Ala Ala Gly Gln Gln	Thr Asn Gln Gln Ala	
210	215	220	225
gca tca ccc gct cag cca	gca gtt gca ttg cca	gtg cag cca tca cct	780
Ala Ser Pro Ala Gln Pro	Ala Val Ala Leu Pro	Val Gln Pro Ser Pro	
230	235	240	
gcc tct gca ggg cct aat	gca aat cct ttg aac	ctt ttt cct cag ggt	828
Ala Ser Ala Gly Pro Asn	Ala Asn Pro Leu Asn	Leu Phe Pro Gln Gly	
245	250	255	
gtt cca agt ggt ggg tcc	aac cca ggt gtt gtt	cca ggt gca gga tct	876
Val Pro Ser Gly Gly Ser	Asn Pro Gly Val Val	Pro Gly Ala Gly Ser	
260	265	270	
ggt gct ctt gat gcc ttg	cga cag ctt cca cag	ttt caa gca ctc ctt	924
Gly Ala Leu Asp Ala Leu	Arg Gln Leu Pro Gln	Phe Gln Ala Leu Leu	
275	280	285	
cag tta gtc cag gct aat	cct caa atc ttg cag	cca atg ctt caa gag	972
Gln Leu Val Gln Ala Asn	Pro Gln Ile Leu Gln	Pro Met Leu Gln Glu	
290	295	300	305
cta ggt aaa caa aac cca	caa att ctg cgg ttg	att cag gaa aat caa	1020
Leu Gly Lys Gln Asn Pro	Gln Ile Leu Arg Leu	Ile Gln Glu Asn Gln	
310	315	320	
gct gag ttt ctc cgc ttg	gtg aat gaa tct cct	gag ggt ggt cct gga	1068
Ala Glu Phe Leu Arg Leu	Val Asn Glu Ser Pro	Glu Gly Gly Pro Gly	
325	330	335	
ggg aac ata cta ggt caa	ctg gca gct gct gtg	cca caa acg ctg aca	1116
Gly Asn Ile Leu Gly Gln	Leu Ala Ala Val Pro	Gln Thr Leu Thr	
340	345	350	

gtt acc cca gag gaa cgg gag gct atc cag cgg ctc gag gga atg ggg	1164
Val Thr Pro Glu Glu Arg Glu Ala Ile Gln Arg Leu Glu Gly Met Gly	
355 360 365	
ttc aac cgt gag ctt gtg cta gaa gtt ttc ttt gca tgc aac aag gac	1212
Phe Asn Arg Glu Leu Val Leu Glu Val Phe Phe Ala Cys Asn Lys Asp	
370 375 380 385	
gaa gag ctt aca gcc aac tac ctc ctg gat cat ggc cat gag ttt gac	1260
Glu Glu Leu Thr Ala Asn Tyr Leu Leu Asp His Gly His Glu Phe Asp	
390 395 400	
gat cag cag caa tagacgtggg gtggatggag gaaaccgagg cagttgcaga	1312
Asp Gln Gln	
405	
acagcgagtg tcgttcttat gccctctgcc tgacgagaga tactcggtcg tctatgctat	1372
gctgctgact atcttttatt tccatatata ttgttcgga atgctttcta agtacaatatt	1432
aattcaatat caagcgttac accgtgtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1492
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1522

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 <212> PRT  
 <213> Zea mays

<400> 2

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Thr Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr	
35 40 45	
Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val	
50 55 60	
Ala Glu Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser	
65 70 75 80	
Ser Ser Gly Ala Ser Thr Ala Thr Thr Ala Lys Ala Pro Ala Thr Leu	
85 90 95	
Ala Gln Pro Ala Ala Pro Val Ala Pro Ala Ala Ser Val Ala Arg Thr	
100 105 110	
Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Pro Ser Val	
115 120 125	
Gln Pro Gln Ala Ala Pro Ala Ala Thr Val Ala Ala Thr Asp Asp Ala	
130 135 140	
Asp Val Tyr Ser Gln Ala Ala Ser Asn Leu Val Phe Gly Asn Asn Leu	
145 150 155 160	
Glu Gln Thr Ile Gln Gln Ile Leu Asp Met Gly Gly Gly Thr Trp Glu	
165 170 175	
Arg Asp Thr Val Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro Glu	
180 185 190	
Arg Ala Ile Asp Tyr Leu Tyr Ser Gly Ile Pro Glu Asn Val Glu Ala	
195 200 205	
Gln Pro Val Ala Arg Ala Pro Ala Ala Gly Gln Gln Thr Asn Gln Gln	
210 215 220	
Ala Ala Ser Pro Ala Gln Pro Ala Val Ala Leu Pro Val Gln Pro Ser	
225 230 235 240	
Pro Ala Ser Ala Gly Pro Asn Ala Asn Pro Leu Asn Leu Phe Pro Gln	
245 250 255	

Gly Val Pro Ser Gly Gly Ser Asn Pro Gly Val Val Pro Gly Ala Gly  
260 265 270

Ser Gly Ala Leu Asp Ala Leu Arg Gln Leu Pro Gln Phe Gln Ala Leu  
275 280 285

Leu Gln Leu Val Gln Ala Asn Pro Gln Ile Leu Gln Pro Met Leu Gln  
290 295 300

Glu Leu Gly Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Gln Glu Asn  
305 310 315 320

Gln Ala Glu Phe Leu Arg Leu Val Asn Glu Ser Pro Glu Gly Gly Pro  
325 330 335

Gly Gly Asn Ile Leu Gly Gln Leu Ala Ala Ala Val Pro Gln Thr Leu  
340 345 350

Thr Val Thr Pro Glu Glu Arg Glu Ala Ile Gln Arg Leu Glu Gly Met  
355 360 365

Gly Phe Asn Arg Glu Leu Val Leu Glu Val Phe Phe Ala Cys Asn Lys  
370 375 380

Asp Glu Glu Leu Thr Ala Asn Tyr Leu Leu Asp His Gly His Glu Phe  
385 390 395 400

Asp Asp Gln Gln Gln  
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<210> 3  
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<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (106)...(1209)

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gtgagcctct cctgcatcgg attgtcccg ccccgctag gcgcc atg aag ctg acg 117  
Met Lys Leu Thr  
1

gtg aag acc ctc aag gga acg cac ttc gag atc cgg gtg cag ccc aac 165  
Val Lys Thr Leu Lys Gly Thr His Phe Glu Ile Arg Val Gln Pro Asn  
5 10 15 20

gac acg att atg gct gtg aag aag aat ata gaa gag ata caa ggg aaa 213  
Asp Thr Ile Met Ala Val Lys Lys Asn Ile Glu Glu Ile Gln Gly Lys  
25 30 35

gac agc tat cca tgg ggc caa caa ctg ctg att ttc aat gga aag gtc 261  
Asp Ser Tyr Pro Trp Gly Gln Gln Leu Leu Ile Phe Asn Gly Lys Val  
40 45 50

ttg aaa gat gaa agt aca ttg gaa gag aat aaa gtc aat gag gat ggg 309  
Leu Lys Asp Glu Ser Thr Leu Glu Glu Asn Lys Val Asn Glu Asp Gly  
55 60 65

ttt cta gtt gtc atg ctt agt aag ggt aaa aca tct ggt tca act gga 357  
Phe Leu Val Val Met Leu Ser Lys Gly Lys Thr Ser Gly Ser Thr Gly  
70 75 80

act tca tct tcc cag cac tca aac act cct gca aca agg cag gca cct 405  
Thr Ser Ser Ser Gln His Ser Asn Thr Pro Ala Thr Arg Gln Ala Pro  
85 90 95 100

cct cta gag gcc cca caa caa gct cct caa ccc ccg gtg gca cca att 453



gca aac tat ctc ctt gag cat gct ggt gag gaa gat taagcgggag 1219  
 Ala Asn Tyr Leu Leu Glu His Ala Gly Glu Glu Asp  
 360 365

tagttttcat acgatttttt ttagtaccga gtgacgaaga gttgatatgg agctgacgat 1279  
 catttgaatt gatttcgttg tgcaagactt gtattacata aacattttaa tacatgtagc 1339  
 tgaacatttc agtagaaatg ctacggttg ggtctcccat cggtgacttt cattagcgtg 1399  
 gtggtaaaca tcggttctgc tcctgtcctg tattaacaca agcttggtt gggaggaagc 1459  
 acaaggagct attgccacct agcaaaagga taaaaggagg gatgacgaat tggcgatgtg 1519  
 tttgcgacac gctgccctca agtgtggatg atgagtgcag ataggttgat gactgtgcca 1579  
 aggtgtgcaa gtgtgtaaac gaacgctgcc ttcgtagttc tgacaactgc gacagttctg 1639  
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 aaa 1702

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 <212> PRT  
 <213> Zea mays

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 Ile Gln Gly Lys Asp Ser Tyr Pro Trp Gly Gln Gln Leu Leu Ile Phe  
 35 40 45  
 Asn Gly Lys Val Leu Lys Asp Glu Ser Thr Leu Glu Glu Asn Lys Val  
 50 55 60  
 Asn Glu Asp Gly Phe Leu Val Val Met Leu Ser Lys Gly Lys Thr Ser  
 65 70 75 80  
 Gly Ser Thr Gly Thr Ser Ser Ser Gln His Ser Asn Thr Pro Ala Thr  
 85 90 95  
 Arg Gln Ala Pro Pro Leu Glu Ala Pro Gln Gln Ala Pro Gln Pro Pro  
 100 105 110  
 Val Ala Pro Ile Thr Thr Ser Gln Pro Glu Gly Leu Pro Ala Gln Ala  
 115 120 125  
 Pro Asn Thr His Asp Asn Ala Ser Asn Leu Leu Ser Gly Arg Asn  
 130 135 140  
 Val Asp Thr Ile Ile Asn Gln Leu Met Glu Met Gly Gly Gly Ser Trp  
 145 150 155 160  
 Asp Lys Asp Lys Val Gln Arg Ala Leu Arg Ala Ala Tyr Asn Asn Pro  
 165 170 175  
 Glu Arg Ala Val Glu Tyr Leu Tyr Ser Gly Ile Pro Val Thr Ala Glu  
 180 185 190  
 Ile Ala Val Pro Ile Gly Gly Gln Gly Ala Asn Thr Thr Asp Arg Ala  
 195 200 205  
 Pro Thr Gly Glu Ala Gly Leu Ser Gly Ile Pro Asn Thr Ala Pro Leu  
 210 215 220  
 Asp Leu Phe Pro Gln Gly Ala Ser Asn Ala Gly Gly Gly Ala Gly Gly  
 225 230 235 240  
 Gly Pro Leu Asp Phe Leu Arg Asn Asn Pro Gln Phe Gln Ala Val Arg  
 245 250 255  
 Glu Met Val His Thr Asn Pro Gln Ile Leu Gln Pro Met Leu Val Glu  
 260 265 270  
 Leu Ser Lys Gln Asn Pro Gln Ile Leu Arg Leu Ile Glu Glu Asn His  
 275 280 285  
 Asp Glu Phe Leu Gln Leu Leu Asn Glu Pro Phe Glu Gly Gly Glu Gly  
 290 295 300  
 Asp Phe Leu Asp Gln Pro Glu Glu Asp Glu Met Pro His Ala Ile Ser

305					310					315					320
Val	Thr	Pro	Glu	Glu	Gln	Glu	Ala	Ile	Gly	Arg	Leu	Glu	Ser	Met	Gly
				325					330					335	
Phe	Asp	Arg	Ala	Arg	Val	Ile	Glu	Ala	Phe	Leu	Ala	Cys	Asp	Arg	Asn
			340					345					350		
Glu	Glu	Leu	Ala	Ala	Asn	Tyr	Leu	Leu	Glu	His	Ala	Gly	Glu	Glu	Asp
		355					360					365			

<210> 5

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based upon an adaptor used for cDNA library construction and poly(dT) to remove clones which have a poly(A) tail but no cDNA insert.

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tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa  
36